

## SEQUENCE LISTING

<110> Curtis, Rory A.J.

<120> 56201, A NOVEL HUMAN SODIUM ION CHANNEL  
FAMILY MEMBER AND USES THEREOF

<130> 10448-060001

<150> US 60/209,238

<151> 2000-06-05

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1356

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)...(1263)

<400> 1

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      Met Ser Gln His Arg His Gln Arg His Ser Arg Val Ile Ser
            1             5             10

agt tca cca gtt gac act aca tcg gtg gga ttt tgc cca aca ttc aag      159
Ser Ser Pro Val Asp Thr Thr Ser Val Gly Phe Cys Pro Thr Phe Lys
 15             20             25             30

aaa ttt aag agg aac gat gat gaa tgt cgg gca ttt gtg aag aga gtc      207
Lys Phe Lys Arg Asn Asp Asp Glu Cys Arg Ala Phe Val Lys Arg Val
      35             40             45

ata atg agc cgt ttc ttt aag ata att atg att agc act gtc aca tcg      255
Ile Met Ser Arg Phe Phe Lys Ile Ile Met Ile Ser Thr Val Thr Ser
      50             55             60

aat gcg ttt ttt atg gcc ttg tgg acc agt tat gac ata agg tac cgc      303
Asn Ala Phe Phe Met Ala Leu Trp Thr Ser Tyr Asp Ile Arg Tyr Arg
      65             70             75

ttg ttc aga ctt ctt gag ttc tcg gag atc ttc ttt gtg tcc atc tgc      351
Leu Phe Arg Leu Leu Glu Phe Ser Glu Ile Phe Phe Val Ser Ile Cys
      80             85             90

aca tct gag ttg tcc atg aag gtc tat gtg gac ccc atc aac tac tgg      399
Thr Ser Glu Leu Ser Met Lys Val Tyr Val Asp Pro Ile Asn Tyr Trp
      95             100             105             110

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aag aac ggc tac aac ctg ctg gat gtg atc att atc atc gtt atg ttt	447
Lys Asn Gly Tyr Asn Leu Leu Asp Val Ile Ile Ile Ile Val Met Phe	
115 120 125	
tta ccc tat gcc ctc cgc cag ctc atg ggc aaa cag ttc act tac ctg	495
Leu Pro Tyr Ala Leu Arg Gln Leu Met Gly Lys Gln Phe Thr Tyr Leu	
130 135 140	
tat atc gct gat ggc atg cag tcc ctg cgc atc ctc aag ctt atc ggc	543
Tyr Ile Ala Asp Gly Met Gln Ser Leu Arg Ile Leu Lys Leu Ile Gly	
145 150 155	
tat agc cag ggc atc cgg acg ctg atc acc gcc gtg ggg cag aca gtc	591
Tyr Ser Gln Gly Ile Arg Thr Leu Ile Thr Ala Val Gly Gln Thr Val	
160 165 170	
tac acc gtg gcc tct gtg ctc ctc ctg ctc ttc ctc ctc atg tac atc	639
Tyr Thr Val Ala Ser Val Leu Leu Leu Leu Phe Leu Leu Met Tyr Ile	
175 180 185 190	
ttc gct atc ttg ggc ttc tgc ctg ttt gga tct cca gac aat ggt gac	687
Phe Ala Ile Leu Gly Phe Cys Leu Phe Gly Ser Pro Asp Asn Gly Asp	
195 200 205	
cat gat aac tgg ggg aac ctg gct gca gct ttt ttc acc ctc ttc agc	735
His Asp Asn Trp Gly Asn Leu Ala Ala Ala Phe Phe Thr Leu Phe Ser	
210 215 220	
ttg gcc acg gtt gat ggc tgg aca gac ctg cag aag cag ttg gac aat	783
Leu Ala Thr Val Asp Gly Trp Thr Asp Leu Gln Lys Gln Leu Asp Asn	
225 230 235	
cgg gaa ttt gct ttg agc cgg gca ttc acc atc atc ttc atc ttg ctc	831
Arg Glu Phe Ala Leu Ser Arg Ala Phe Thr Ile Ile Phe Ile Leu Leu	
240 245 250	
gcc tct ttc atc ttc ctc aac atg ttc gtg ggt gtg atg atc atg cac	879
Ala Ser Phe Ile Phe Leu Asn Met Phe Val Gly Val Met Ile Met His	
255 260 265 270	
aca gag gac tcc atc aga aag ttt gag cga gag ctg atg ttg gag cag	927
Thr Glu Asp Ser Ile Arg Lys Phe Glu Arg Glu Leu Met Leu Glu Gln	
275 280 285	
cag gag atg ctc atg gga gag aag cag gtg att ctg cag cgg cag cag	975
Gln Glu Met Leu Met Gly Glu Lys Gln Val Ile Leu Gln Arg Gln Gln	
290 295 300	
gag gag atc agc agg ctg atg cac ata cag aaa aat gct gac tgc aca	1023
Glu Glu Ile Ser Arg Leu Met His Ile Gln Lys Asn Ala Asp Cys Thr	
305 310 315	
agt ttc agt gag ctg gtg gag aac ttt aag aag acc ttg agc cac act	1071
Ser Phe Ser Glu Leu Val Glu Asn Phe Lys Lys Thr Leu Ser His Thr	
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			20					25					30		
Lys	Arg	Asn	Asp	Asp	Glu	Cys	Arg	Ala	Phe	Val	Lys	Arg	Val	Ile	Met
		35				40						45			
Ser	Arg	Phe	Phe	Lys	Ile	Ile	Met	Ile	Ser	Thr	Val	Thr	Ser	Asn	Ala
	50					55					60				
Phe	Phe	Met	Ala	Leu	Trp	Thr	Ser	Tyr	Asp	Ile	Arg	Tyr	Arg	Leu	Phe
65					70					75					80
Arg	Leu	Leu	Glu	Phe	Ser	Glu	Ile	Phe	Phe	Val	Ser	Ile	Cys	Thr	Ser
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Glu	Leu	Ser	Met	Lys	Val	Tyr	Val	Asp	Pro	Ile	Asn	Tyr	Trp	Lys	Asn
			100					105					110		
Gly	Tyr	Asn	Leu	Leu	Asp	Val	Ile	Ile	Ile	Ile	Val	Met	Phe	Leu	Pro
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Tyr	Ala	Leu	Arg	Gln	Leu	Met	Gly	Lys	Gln	Phe	Thr	Tyr	Leu	Tyr	Ile
	130					135					140				
Ala	Asp	Gly	Met	Gln	Ser	Leu	Arg	Ile	Leu	Lys	Leu	Ile	Gly	Tyr	Ser
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Gln	Gly	Ile	Arg	Thr	Leu	Ile	Thr	Ala	Val	Gly	Gln	Thr	Val	Tyr	Thr
				165					170					175	
Val	Ala	Ser	Val	Leu	Leu	Leu	Leu	Phe	Leu	Leu	Met	Tyr	Ile	Phe	Ala
			180					185					190		
Ile	Leu	Gly	Phe	Cys	Leu	Phe	Gly	Ser	Pro	Asp	Asn	Gly	Asp	His	Asp
		195					200					205			
Asn	Trp	Gly	Asn	Leu	Ala	Ala	Ala	Phe	Phe	Thr	Leu	Phe	Ser	Leu	Ala
	210					215					220				
Thr	Val	Asp	Gly	Trp	Thr	Asp	Leu	Gln	Lys	Gln	Leu	Asp	Asn	Arg	Glu
225					230					235					240
Phe	Ala	Leu	Ser	Arg	Ala	Phe	Thr	Ile	Ile	Phe	Ile	Leu	Leu	Ala	Ser
				245					250					255	
Phe	Ile	Phe	Leu	Asn	Met	Phe	Val	Gly	Val	Met	Ile	Met	His	Thr	Glu

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                260                265                270
Asp Ser Ile Arg Lys Phe Glu Arg Glu Leu Met Leu Glu Gln Gln Glu
      275                280                285
Met Leu Met Gly Glu Lys Gln Val Ile Leu Gln Arg Gln Gln Glu Glu
      290                295                300
Ile Ser Arg Leu Met His Ile Gln Lys Asn Ala Asp Cys Thr Ser Phe
305                310                315                320
Ser Glu Leu Val Glu Asn Phe Lys Lys Thr Leu Ser His Thr Asp Pro
      325                330                335
Met Val Leu Asp Asp Phe Gly Thr Ser Leu Pro Phe Ile Asp Ile Tyr
      340                345                350
Phe Ser Thr Leu Asp Tyr Gln Asp Thr Thr Val His Lys Leu Gln Glu
      355                360                365
Leu Tyr Tyr Glu Ile Val His Val Leu Ser Leu Met Leu Glu Asp Leu
      370                375                380
Pro Gln Glu Lys Pro Gln Ser Leu Glu Lys Val Asp Glu Lys
385                390                395

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<210> 3

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 3

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gcattttgtga agagagtcac aatgagccgt ttctttaaga taattatgat tagcactgtc      180
acatcgaatg cgttttttat ggccttgtgg accagttatg acataaggta ccgcttggtc      240
agacttcttg agttctcgga gatcttcttt gtgtccatct gcacatctga gttgtccatg      300
aaggtctatg tggaccccat caactactgg aagaacggct acaacctgct ggatgtgatc      360
attatcatcg ttatgttttt accctatgcc ctccgccagc tcatgggcaa acagttcact      420
tacctgtata tcgctgatgg catgcagtc ctgcgcaccc tcaagcttat cggctatagc      480
cagggcatcc ggacgctgat caccgccgtg gggcagacag tctacaccgt ggcctctgtg      540
ctcctcctgc tcttcctcct catgtacatc ttcgctatct tgggcttctg cctgtttgga      600
tctccagaca atggtgacca tgataactgg gggaaacctg ctgcagcttt ttccaccctc      660
ttcagcttgg ccacggttga tggctggaca gacctgcaga agcagttgga caatcgggaa      720
tttgctttga gccgggcatc caccatcatc ttcatcttgc tcgcctcttt catcttcctc      780
aacatgttcg tgggtgtgat gatcatgcac acagaggact ccatcagaaa gtttgagcga      840
gagctgatgt tggagcagca ggagatgctc atgggagaga agcaggtgat tctgcagcgg      900
cagcaggagg agatcagcag gctgatgcac atacagaaaa atgctgactg cacaagtttc      960
agtgaagctgg tggagaactt taagaagacc ttgagccaca ctgacccaat ggtcttggat      1020
gattttggca ctagcttacc ctccatcgat atctactttt ccactctgga ctaccaggac      1080
acaactgtcc acaagcttca agagctgtac tatgagatcg tgcagtgctg gagcctaata      1140
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<210> 4

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

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Leu Asn Asp Asp Lys Val Ser Lys Thr Ile Ala Leu Ala Met Glu His

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      20      25      30
Pro Asn Gln Glu Thr Leu Asn Asp Ile Leu Asp Tyr Val Glu Tyr Val
      35      40      45
Phe Thr Gly Ile Phe Thr Phe Glu Met Leu Leu Lys Met Ile Ala Leu
      50      55      60
Gly Phe Lys Leu His Lys Gly Ala Tyr Phe Arg Asn Gly Trp Asn Ile
      65      70      75      80
Leu Asp Phe Val Val Val Leu Leu Ser Ile Ile Glu Leu Gly Leu Ser
      85      90      95
Leu Ile Asn Lys Lys Ala Ala Asn Val Gly Gly Ser Pro Gln Gln Ala
      100      105      110
Lys Gly Ser Leu Phe Gly Leu Lys Val Leu Arg Leu Phe Arg Val Leu
      115      120      125
Arg Pro Leu Lys Leu Val Arg Arg Ala Pro Gly Leu Arg Val Leu Val
      130      135      140
Gln Thr Leu Leu Asn Ser Met Lys Ala Leu Gly Asn Leu Leu Leu Leu
      145      150      155      160
Leu Phe Leu Phe Val Phe Ile Phe Ala Ile Ile Gly Met Gln Leu Phe
      165      170      175
Ala Gly Lys Phe Glu Phe Asp Cys Ile Asp Glu Ser Thr Glu Leu Phe
      180      185      190
Asp Ile Ile Ala Thr Glu Pro Ser Leu Cys Gly Asn Glu Ser Tyr Ala
      195      200      205
Arg Asp Cys Pro Asp Gly Tyr Thr Cys Arg Arg Gly Trp Glu Gly Pro
      210      215      220
Asn Asn Gly Arg Thr Asn Phe Asp Asn Phe Pro Gln Ala Phe Leu Thr
      225      230      235      240
Leu Phe Gln Val Met Thr Gly Glu Gly Trp Gly Asp Val Leu Tyr Asp
      245      250      255
Thr Ile Asp Ala Ala Gly Glu Asp Cys Asp Pro Glu Ser Glu Ala Gly
      260      265      270
Gly Gly Ile Cys Gly Asn Asn Val Leu Met Gly Ile Tyr Phe Ile Ser
      275      280      285
Leu Ile Ile Leu Gly Ser Phe Leu Thr Leu Asn Leu Phe Leu Ala Val
      290      295      300
Ile
305

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<210> 5

<211> 1836

<212> PRT

<213> Homo sapiens

<400> 5

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      20      25      30
Val Glu Glu Glu Ala Arg Leu Gln Arg Asn Lys Gln Met Glu Ile Glu
      35      40      45
Glu Pro Glu Arg Lys Pro Arg Ser Asp Leu Glu Ala Gly Lys Asn Leu
      50      55      60
Pro Met Ile Tyr Gly Asp Pro Pro Pro Glu Val Ile Gly Ile Pro Leu
      65      70      75      80
Glu Asp Leu Asp Pro Tyr Tyr Ser Asn Lys Lys Thr Phe Ile Val Leu
      85      90      95
Asn Lys Gly Lys Ala Ile Phe Arg Phe Ser Ala Thr Pro Ala Leu Tyr

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100	105	110
Leu Leu Ser Pro Phe Ser Val Val Arg Arg Gly Ala Ile Lys Val Leu		
115	120	125
Ile His Ala Leu Phe Ser Met Phe Ile Met Ile Thr Ile Leu Thr Asn		
130	135	140
Cys Val Phe Met Thr Met Ser Asp Pro Pro Pro Trp Ser Lys Asn Val		
145	150	155
Glu Tyr Thr Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile		
165	170	175
Leu Ala Arg Gly Phe Cys Val Asp Asp Phe Thr Phe Leu Arg Asp Pro		
180	185	190
Trp Asn Trp Leu Asp Phe Ser Val Ile Met Met Ala Tyr Leu Thr Glu		
195	200	205
Phe Val Asp Leu Gly Asn Ile Ser Ala Leu Arg Thr Phe Arg Val Leu		
210	215	220
Arg Ala Leu Lys Thr Ile Thr Val Ile Pro Gly Leu Lys Thr Ile Val		
225	230	235
Gly Ala Leu Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu		
245	250	255
Thr Val Phe Cys Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe		
260	265	270
Met Gly Asn Leu Arg Gln Lys Cys Val Arg Trp Pro Pro Pro Phe Asn		
275	280	285
Asp Thr Asn Thr Thr Trp Tyr Ser Asn Asp Thr Trp Tyr Gly Asn Asp		
290	295	300
Thr Trp Tyr Gly Asn Glu Met Trp Tyr Gly Asn Asp Ser Trp Tyr Ala		
305	310	315
Asn Asp Thr Trp Asn Ser His Ala Ser Trp Ala Thr Asn Asp Thr Phe		
325	330	335
Asp Trp Asp Ala Tyr Ile Ser Asp Glu Gly Asn Phe Tyr Phe Leu Glu		
340	345	350
Gly Ser Asn Asp Ala Leu Leu Cys Gly Asn Ser Ser Asp Ala Gly His		
355	360	365
Cys Pro Gln Gly Tyr Glu Cys Ile Lys Thr Gly Arg Asn Pro Asn Tyr		
370	375	380
Gly Tyr Thr Ser Tyr Asp Thr Phe Ser Trp Ala Phe Leu Ala Leu Phe		
385	390	395
Arg Leu Met Thr Gln Asp Tyr Trp Glu Asn Leu Phe Gln Leu Thr Leu		
405	410	415
Arg Ala Ala Gly Lys Thr Tyr Met Ile Phe Phe Val Val Ile Ile Phe		
420	425	430
Leu Gly Ser Phe Tyr Leu Ile Asn Leu Ile Leu Ala Val Val Ala Met		
435	440	445
Ala Tyr Ala Glu Gln Asn Glu Ala Thr Leu Ala Glu Asp Lys Glu Lys		
450	455	460
Glu Glu Glu Phe Gln Gln Met Leu Glu Lys Phe Lys Lys His Gln Glu		
465	470	475
Glu Leu Glu Lys Ala Lys Ala Ala Gln Ala Leu Glu Gly Gly Glu Ala		
485	490	495
Asp Gly Asp Pro Ala His Gly Lys Asp Cys Asn Gly Ser Leu Asp Thr		
500	505	510
Ser Gln Gly Glu Lys Gly Ala Pro Arg Gln Ser Gly Ser Gly Asp Ser		
515	520	525
Gly Ile Ser Asp Ala Met Glu Glu Leu Glu Glu Ala His Gln Lys Cys		
530	535	540
Pro Pro Trp Trp Tyr Lys Cys Ala His Lys Val Leu Ile Trp Asn Cys		
545	550	555
		560

Cys Ala Pro Trp Leu Lys Phe Lys Asn Ile Ile His Leu Ile Val Met  
 565 570 575  
 Asp Pro Phe Val Asp Leu Gly Ile Thr Ile Cys Ile Val Leu Asn Thr  
 580 585 590  
 Leu Phe Met Ala Met Glu His Tyr Pro Met Thr Glu His Phe Asp Asn  
 595 600 605  
 Val Leu Thr Val Gly Asn Leu Val Phe Thr Gly Ile Phe Thr Ala Glu  
 610 615 620  
 Met Val Leu Lys Leu Ile Ala Met Asp Pro Tyr Glu Tyr Phe Gln Gln  
 625 630 635 640  
 Gly Trp Asn Ile Phe Asp Ser Ile Ile Val Thr Leu Ser Leu Val Glu  
 645 650 655  
 Leu Gly Leu Ala Asn Val Gln Gly Leu Ser Val Leu Arg Ser Phe Arg  
 660 665 670  
 Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Met  
 675 680 685  
 Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly Asn Leu Thr  
 690 695 700  
 Leu Val Leu Ala Ile Ile Val Phe Ile Phe Ala Val Val Gly Met Gln  
 705 710 715 720  
 Leu Phe Gly Lys Ser Tyr Lys Glu Cys Val Cys Lys Ile Ala Leu Asp  
 725 730 735  
 Cys Asn Leu Pro Arg Trp His Met His Asp Phe Phe His Ser Phe Leu  
 740 745 750  
 Ile Val Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Thr Met Trp Asp  
 755 760 765  
 Cys Met Glu Val Ala Gly Gln Ala Met Cys Leu Thr Val Phe Leu Met  
 770 775 780  
 Val Met Val Ile Gly Asn Leu Val Val Leu Asn Leu Phe Leu Ala Leu  
 785 790 795 800  
 Leu Leu Ser Ser Phe Ser Ala Asp Ser Leu Ala Ala Ser Asp Glu Asp  
 805 810 815  
 Gly Glu Met Asn Asn Leu Gln Ile Ala Ile Gly Arg Ile Lys Leu Gly  
 820 825 830  
 Ile Gly Phe Ala Lys Ala Phe Leu Leu Gly Leu Leu His Gly Lys Ile  
 835 840 845  
 Leu Ser Pro Lys Asp Ile Met Leu Ser Leu Gly Glu Ala Asp Gly Ala  
 850 855 860  
 Gly Glu Ala Gly Glu Gly Glu Thr Ala Pro Glu Asp Glu Lys Lys  
 865 870 875 880  
 Glu Pro Pro Glu Glu Asp Leu Lys Lys Asp Asn His Ile Leu Asn His  
 885 890 895  
 Met Gly Leu Ala Asp Gly Pro Pro Ser Ser Leu Glu Leu Asp His Leu  
 900 905 910  
 Asn Phe Ile Asn Asn Pro Tyr Leu Thr Ile Gln Val Pro Ile Ala Ser  
 915 920 925  
 Glu Glu Ser Asp Leu Glu Met Pro Thr Glu Glu Glu Thr Asp Thr Phe  
 930 935 940  
 Ser Glu Pro Glu Asp Ser Lys Lys Pro Pro Gln Pro Leu Tyr Asp Gly  
 945 950 955 960  
 Asn Ser Ser Val Cys Ser Thr Ala Asp Tyr Lys Pro Pro Glu Glu Asp  
 965 970 975  
 Pro Glu Glu Gln Ala Glu Glu Asn Pro Glu Gly Glu Gln Pro Glu Glu  
 980 985 990  
 Cys Phe Thr Glu Ala Cys Val Gln Arg Trp Pro Cys Leu Tyr Val Asp  
 995 1000 1005  
 Ile Ser Gln Gly Arg Gly Lys Lys Trp Trp Thr Leu Arg Arg Ala Cys

1010	1015	1020
Phe Lys Ile Val Glu His Asn Trp Phe Glu Thr Phe Ile Val Phe Met		
1025	1030	1035
Ile Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Ile Glu		1040
	1045	1050
Gln Arg Arg Val Ile Arg Thr Ile Leu Glu Tyr Ala Asp Lys Val Phe		1055
	1060	1065
Thr Tyr Ile Phe Ile Met Glu Met Leu Leu Lys Trp Val Ala Tyr Gly		1070
	1075	1080
Phe Lys Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile		1085
	1090	1095
Val Asp Val Ser Ile Ile Ser Leu Val Ala Asn Trp Leu Gly Tyr Ser		1100
1105	1110	1115
Glu Leu Gly Pro Ile Lys Ser Leu Arg Thr Leu Arg Ala Leu Arg Pro		1120
	1125	1130
Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val Lys Pro		1135
	1140	1145
Leu Leu Gly Ala Ile Pro Ser Ile Met Asn Val Leu Leu Val Cys Leu		1150
	1155	1160
Ile Phe Trp Leu Ile Phe Ser Ile Met Gly Val Asn Leu Phe Ala Gly		1165
	1170	1175
Lys Phe Tyr Tyr Cys Ile Asn Thr Thr Thr Ser Glu Arg Phe Asp Ile		1180
1185	1190	1195
Ser Glu Val Asn Asn Lys Ser Glu Cys Glu Ser Leu Met His Thr Gly		1200
	1205	1210
Gln Val Arg Trp Leu Asn Val Lys Val Asn Tyr Asp Asn Val Gly Leu		1215
	1220	1225
Gly Tyr Leu Ser Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp		1230
	1235	1240
Ile Met Tyr Ala Ala Val Asp Ser Arg Glu Lys Glu Glu Gln Pro Gln		1245
	1250	1255
Tyr Glu Val Asn Leu Tyr Met Tyr Leu Tyr Phe Val Ile Phe Ile Ile		1260
1265	1270	1275
Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile Asp		1280
	1285	1290
Asn Phe Asn Gln Gln Lys Lys Lys Leu Gly Gly Lys Asp Ile Phe Met		1295
	1300	1305
Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser		1310
	1315	1320
Lys Lys Pro Gln Lys Lys Pro Ile Pro Arg Pro Gln Asn Lys Ile Gln Gly		1325
	1330	1335
Met Val Tyr Asp Leu Val Thr Lys Gln Ala Phe Asp Ile Thr Ile Met		1340
1345	1350	1355
Ile Leu Ile Cys Leu Asn Met Val Thr Met Met Val Glu Thr Asp Asp		1360
	1365	1370
Gln Ser Gln Leu Lys Val Asp Ile Leu Tyr Asn Ile Asn Met Ile Phe		1375
	1380	1385
Ile Ile Ile Phe Thr Gly Glu Cys Val Leu Lys Met Leu Ala Leu Arg		1390
	1395	1400
Gln Tyr Tyr Phe Thr Val Gly Trp Asn Ile Phe Asp Phe Val Val Val		1405
	1410	1415
Ile Leu Ser Ile Val Gly Leu Ala Leu Ser Asp Leu Ile Gln Lys Tyr		1420
1425	1430	1435
Phe Val Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly		1440
	1445	1450
Arg Val Leu Arg Leu Ile Arg Gly Ala Lys Gly Ile Arg Thr Leu Leu		1455
	1460	1465
		1470



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Phe Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu
1475 1480 1485
Leu Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ser Asn Phe
1490 1495 1500
Ala Tyr Val Lys Lys Glu Ser Gly Ile Asp Asp Met Phe Asn Phe Glu
1505 1510 1515 1520
Thr Phe Gly Asn Ser Ile Ile Cys Leu Phe Glu Ile Thr Thr Ser Ala
1525 1530 1535
Gly Trp Asp Gly Leu Leu Asn Pro Ile Leu Asn Ser Gly Pro Pro Asp
1540 1545 1550
Cys Asp Pro Asn Leu Glu Asn Pro Gly Thr Ser Val Lys Gly Asp Cys
1555 1560 1565
Gly Asn Pro Ser Ile Gly Ile Cys Phe Phe Cys Ser Tyr Ile Ile Ile
1570 1575 1580
Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Ile Ile Leu Glu Asn
1585 1590 1595 1600
Phe Asn Val Ala Thr Glu Glu Ser Ser Glu Pro Leu Gly Glu Asp Asp
1605 1610 1615
Phe Glu Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Asp Ala Thr
1620 1625 1630
Gln Phe Ile Ala Tyr Ser Arg Leu Ser Asp Phe Val Asp Thr Leu Gln
1635 1640 1645
Glu Pro Leu Arg Ile Ala Lys Pro Asn Lys Ile Lys Leu Ile Thr Leu
1650 1655 1660
Asp Leu Pro Met Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu
1665 1670 1675 1680
Phe Ala Leu Thr Lys Glu Val Leu Gly Asp Ser Gly Glu Met Asp Ala
1685 1690 1695
Leu Lys Gln Thr Met Glu Glu Lys Phe Met Ala Ala Asn Pro Ser Lys
1700 1705 1710
Val Ser Tyr Glu Pro Ile Thr Thr Thr Leu Lys Arg Lys His Glu Glu
1715 1720 1725
Val Cys Ala Ile Lys Ile Gln Arg Ala Tyr Arg Arg His Leu Leu Gln
1730 1735 1740
Arg Ser Met Lys Gln Ala Ser Tyr Met Tyr Arg His Ser His Asp Gly
1745 1750 1755 1760
Ser Gly Asp Asp Ala Pro Glu Lys Glu Gly Leu Leu Ala Asn Thr Met
1765 1770 1775
Ser Lys Met Tyr Gly His Glu Asn Gly Asn Ser Ser Ser Pro Ser Pro
1780 1785 1790
Glu Glu Lys Gly Glu Ala Gly Asp Ala Gly Pro Thr Met Gly Leu Met
1795 1800 1805
Pro Ile Ser Pro Ser Asp Thr Ala Trp Pro Pro Ala Pro Pro Pro Gly
1810 1815 1820
Gln Thr Val Arg Pro Gly Val Lys Glu Ser Leu Val
1825 1830 1835

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<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<221> VARIANT
<222> 2

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<223> Xaa = any amino acid

<221> VARIANT

$\langle 222 \rangle$  3

<223> Xaa = Asp or Glu

 $\langle 400 \rangle$  6

Thr Xaa Xaa Gly Trp  
1 5

1

5

Table 1	
Summary of the study	
Study design	Retrospective cohort study
Study period	1990-1999
Study location	United States
Study population	1,000,000
Study variables	Age, sex, race, education, income, occupation, health status, lifestyle factors, environmental factors, social factors, genetic factors, clinical factors, laboratory factors, imaging factors, treatment factors, outcome factors
Study results	See text for details
Study conclusions	See text for details